#4


```
                 9           18          27          36          45          54
5' GGC TTC TGG GAG CNA CCG CTC CGC TCG TCT CGT TGG TTC CGG AGG TCG CTG CGG

                63          72          81          90          99         108
   CGG TGG GAA ATG CTG GCG CGC GCG GCG CGG GGG CAC TGG GGC CCT TTT GCT GAG
               M   L   A   R   A   A   R   G   H   W   G   P   F   A   E

               117         126         135         144         153         162
   GGG CTC TCT ACT GGC TTC TGG CCG CGC TCC GGC CGC GCC TCC TCT GGA TTG CCC
   G   L   S   T   G   F   W   P   R   S   G   R   A   S   S   G   L   P

               171         180         189         198         207         216
   CGA AAC ACC GTG GTA CTG TTC GTG CCG CAG CAG GAG GCC TGG GTG GTG GAG CGA
   R   N   T   V   V   L   F   V   P   Q   Q   E   A   W   V   V   E   R

               225         234         243         252         261         270
   ATG GGC CGA TTC CAC CGG ATC CTG GAG CCT GGT TTG AAC ATC CTC ATC CCT GTG
   M   G   R   F   H   R   I   L   E   P   G   L   N   I   L   I   P   V

               279         288         297         306         315         324
   TTA GAC CGG ATC CGA TAT GTG CAG AGT CTC AAG GAA ATT GTC ATC AAC GTG CCT
   L   D   R   I   R   Y   V   Q   S   L   K   E   I   V   I   N   V   P

               333         342         351         360         369         378
   GAG CAG TCG GCT GTG ACT CTC GAC AAT GTA ACT CTG CAA ATC GAT GGA GTC CTT
   E   Q   S   A   V   T   L   D   N   V   T   L   Q   I   D   G   V   L
```

FIGURE 1A

```
          387         396         405         414         423         432
TAC CTG CGC ATC ATG GAC CCT TAC AAG GCA AGC TAC GGT GTG GAG GAC CCT GAG
Y   L   R   I   M   D   P   Y   K   A   S   Y   G   V   E   D   P   E

          441         450         459         468         477         486
TAT GCC GTC ACC CAG CTA GCT CAA ACA ACC ATG AGA TCA GAG CTC GGC AAA CTC
Y   A   V   T   Q   L   A   Q   T   T   M   R   S   E   L   G   K   L

          495         504         513         522         531         540
TCT NTG GAC AAA GTC TTC CGG GAA CGG GAG TCC CTG AAT GCC AGC ATT GTG GAT
S   X   D   K   V   F   R   E   R   E   S   L   N   A   S   I   V   D

          549         558         567         576         585         594
GCC ATC AAC CAA GCT GCT GAC TGC TGG GGT ATC CGC TGC CTN CGT TAT GAG ATC
A   I   N   Q   A   A   D   C   W   G   I   R   C   L   R   Y   E   I

          603         612         621         630         639         648
AAG GAT ATC CAT GTG CCA CCC CGG GTG AAA GAG TCT ATG CAG ATG CAG GTG GAG
K   D   I   H   V   P   P   R   V   K   E   S   M   Q   M   Q   V   E

          657         666         675         684         693         702
GCA GAG CGG CGG AAA CGG GCC ACA GTT CTA GAG TCT GAG GGG ACC CGA GAG TCG
A   E   R   R   K   R   A   T   V   L   E   S   E   G   T   R   E   S

          711         720         729         738         747         756
GCC ATC AAT GTG GCA GAA GGG AAG AAA CAG GCC CAG ATC CTG GCC TCC GAA GCA
A   I   N   V   A   E   G   K   K   Q   A   Q   I   L   A   S   E   A
```

FIGURE 1B

```
        765         774         783         792         801         810
GAA AAG GCT GAA CAG ATA AAT CAG GCA GCA GGA GAG GCC AGT GCA GTT CTG GCG
E   K   A   E   Q   I   N   Q   A   A   G   E   A   S   A   V   L   A

        819         828         837         846         855         864
AAG GCC AAG GCT AAA GCT GAA GCT ATT CGA ATC CTG GCT GCA GCT CTG ACA CAA
K   A   K   A   K   A   E   A   I   R   I   L   A   A   A   L   T   Q

        873         882         891         900         909         918
CAT AAT GGA GAT GCA GCA GCT TCA CTG ACT GTG GCC GAG CAG TAT GTC AGC GCG
H   N   G   D   A   A   A   S   L   T   V   A   E   Q   Y   V   S   A

        927         936         945         954         963         972
TTC TCC AAA CTG GCC AAG GAC TCC AAC ACT ATC CTA CTG CCC TCC AAC CCT GGC
F   S   K   L   A   K   D   S   N   T   I   L   L   P   S   N   P   G

        981         990         999        1008        1017        1026
GAT GTC ACC AGC ATG GTG GCT CAG GCC ATG GGT GTA TAT GGA GCC CTC ACC AAA
D   V   T   S   M   V   A   Q   A   M   G   V   Y   G   A   L   T   K

       1035        1044        1053        1062        1071        1080
GCC CCA GTG CCA GGG ACT CCA GAC TCA CTC TCC AGT GGG AGC AGC AGA GAT GTC
A   P   V   P   G   T   P   D   S   L   S   S   G   S   S   R   D   V

       1089        1098        1107        1116        1125        1134
CAG GGT ACA GAT GCA AGT NTT GAT GAG GAA CTT GAT CGA GTC AAG ATG AGT TAG
Q   G   T   D   A   S   X   D   E   E   L   D   R   V   K   M   S   *
```

FIGURE 1C

```
          1143        1152        1161        1170        1179        1188
TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT
3'
```

FIGURE 1D

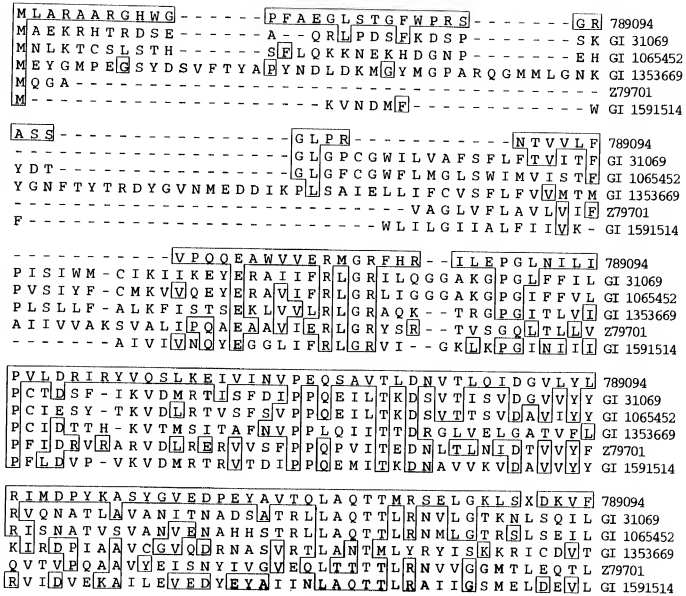
1 MLARAARGHWG------PFAEGLSTGFWPRS-------GR 789094
1 MAEKRHTRDSE------A--QRLPDSFKDSP--------SK GI 31069
1 MNLKTCSLSTH------SFLQKKNEKHDGNP--------EH GI 1065452
1 MEYGMPEGSYDSVFTYAPYNDLDKMGYMGPARQGMMLGNK GI 1353669
1 MQGA---------- Z79701
1 M----------KVNDMF----------W GI 1591514
28 ASS----------GLPR----------NTVVLF 789094
26 ----------GLGPCGWILVAFSFLFTVITF GI 31069
28 YDT----------GLGFCGWFLMGLSWIMVISTF GI 1065452
41 YGNFTYTRDYGVNMEDDIKPLSAIELLIFCVSFLFVVMTM GI 1353669
5 ----------VAGLVFLAVLVIF Z79701
9 F----------WLILGIIALFIIVK- GI 1591514
41 ----------VPQQEAWVVERMGRFHR--ILEPGLNILI 789094
47 PISIWM-CIKIIKEYERAIIFRLGRILQGGAKGPGLFFIL GI 31069
52 PVSIYF-CMKVVQEYERAVIFRLGRLIGGGAKGPGIFFVL GI 1065452
81 PLSLLF-ALKFISTSEKLVVLRLGRAQK--TRGPGITLVI GI 1353669
18 AIIVVAKSVALIPQAEAAVIERLGRYSR--TVSGQLTLLV Z79701
24 -------AIVIVNQYEGGLIFRLGRVI--GKLKPGINIII GI 1591514
68 PVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYL 789094
86 PCTDSF-IKVDMRTISFDIPPQEILTKDSVTISVDGVVYY GI 31069
91 PCIESY-TKVDLRTVSFSVPPQEILTKDSVTTSVDAVIYY GI 1065452
118 PCIDTTH-KVTMSITAFNVPPLQIITTDRGLVELGATVFL GI 1353669
56 PFIDRVRARVDLRERVVSFPPQPVITEDNLTLNIDTVVYF Z79701
55 PFLDVP-VKVDMRTRVTDIPPQEMITKDNAVVKVDAVVYY GI 1591514
108 RIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVF 789094
125 RVQNATLAVANITNADSATRLLAQTTLRNVLGTKNLSQIL GI 31069
130 RISNATVSVANVENAHHSTRLLAQTTLRNMLGTRSLSEIL GI 1065452
157 KIRDPIAAVCGVQDRNASVRTLANTMLYRYISKKRICDVT GI 1353669
96 QVTVLPQAAVYEISNYIVGVEQLTTTTLRNVVGGMTLEQTL Z79701
94 RVIDVEKAILEVEDYEYAIINLAQTTLRAIIGSMELDEVL GI 1591514

FIGURE 2A

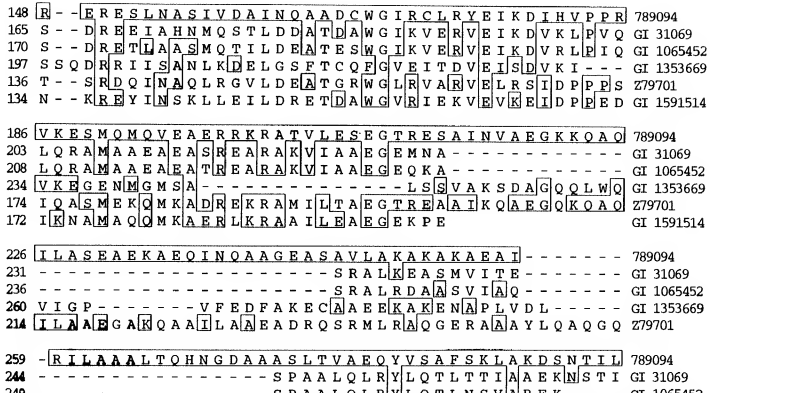

FIGURE 2B

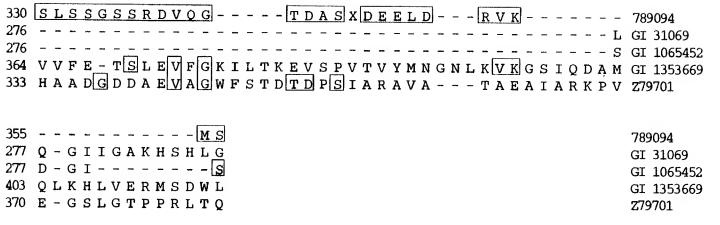

FIGURE 2C

Library	Lib Description	Abun	Pct Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577
TESTNOT03	testis, 37 M	1	0.0557
LIVRNOT02	liver, 32 F	1	0.0515
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418
LVENNOT03	heart, left ventricle, 31 M	1	0.0336
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288
KERANOT01	keratinocytes, neonatal M	1	0.0227
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194
LUNGNOT04	lung, 2 M	1	0.0182
PGANNOT01	paraganglia, 46 M	1	0.0159
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150

FIGURE 3